Claims:

1. A method for determining the global fold of a peptidic molecule having a sequence of three or greater amino acids which comprises the steps of:

(a) providing said molecule in a form which is substituted on the backbone with an isotope selected from the group consisting of ^{13}C, ^{15}N, and both ^{13}C and ^{15}N;

(b) subjecting said substituted molecule to NMR analysis in a non-aligned medium;

(c) assigning said molecule by computer based on said NMR analysis;

(d) placing said molecule in a first state of partial alignment and measuring residual dipolar couplings for said molecule in said first state of partial alignment, wherein the magnitudes and orientations of the principle axes of the alignment tensors for said first state of partial alignment are known or obtained;

(e) placing said molecule in a second state of partial alignment and measuring residual dipolar couplings for said molecule in said second state of partial alignment, wherein the magnitudes and orientations of the principle axes of the alignment tensors for said second state of partial alignment are known or obtained;

(f) varying computationally by increments the φ,ψ angles for a first amino acid of said molecule;

(g) minimizing the rigid-body orientation of said first amino acid and a second amino acid adjacent in the peptidic

sequence to said first amino acid with respect to both tensor frames simultaneously;

(h) calculating the minimum difference between measured and calculated dipolar couplings for each of said first and second amino acids;

(i) deriving the φ,ψ angles and orientation of the dipeptide fragment composed of said first and second amino acids; and

(j) repeating steps (f)-(i) for each sequential dipeptide fragment of said molecule to obtain a global fold of said peptidic molecule.

2. The method according to claim 1 which further comprises repeating steps (f)-(i) for at least one secondary structural element.

3. The method according to claim 1 which comprises providing said molecule in a form in which the Cα position protons are isotopically substituted with ^2H.

4. The method according to claim 1, wherein the residual dipolar couplings for said molecule are measured in step (d) in at least two different media which impart a weak alignment to said molecule.

5. The method according to claim 4, wherein said media which impart a weak alignment on said molecule are liquid crystalline solutions.

6. The method according to claim 1 which further comprises additionally performing steps (b) through (j) using said peptidic molecule which has been universally isotopically substituted with ^{13}C, ^{15}N, or both ^{13}C and ^{15}N in one or more species of amino acid.

7. The method according to claim 6, wherein said peptidic molecule is universally isotopically substituted with ^{13}C, ^{15}N, or both ^{13}C and ^{15}N in one species of amino acid.

8. The method according to claim 1, which further comprises refining said global fold of said peptidic molecule by including data concerning interatom distances.

9. The method according to claim 8, wherein said data concerning interatom distances is NOE data.

10. A method according to claim 1, wherein at least three residual dipolar couplings are measured for each state of partial alignment.

11. A method according to claim 10, wherein three residual dipolar couplings are measured for each state of partial alignment.

12. A method according to claim 10, wherein four residual dipolar couplings are measured for each state of partial alignment.

13. A method according to claim 10, wherein five residual dipolar couplings are measured for each state of partial alignment.

14. A method according to claim 10, wherein more than five residual dipolar couplings are measured for each state of partial alignment.

15. A structural map obtained by the method of any one of claims 1-14.